

10/572711

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SEQUENCE LISTING

<110> Bogosian, Gregg
O'Neill, Julia P.
Smith, Hong Q.

<120> Prevention of Incorporation of Non-Standard Amino Acids into Protein

<130> 11916.0059.PCUS01

<150> PCT/US 2004/031224

<151> 2004-09-23

<150> US 60/505,807

<151> 2003-09-25

<160> 16

<170> PatentIn version 3.3

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<211> 1344

<212> DNA

<213> Escherichia coli

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Thr Thr Leu Trp Pro Phe Leu Glu Gln Asn Pro Lys Tyr Arg Gln Met
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Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg
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Val Val Trp Val Asp Asp Arg Asn Gln Ile Gln Val Asn Arg Ala Trp
65              70              75              80

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Arg Val Gln Phe Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Met Arg
          85              90              95

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Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu
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Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys
115              120              125

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Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Gly Glu Val Met
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Arg Phe Cys Gln Ala Leu Met Thr Glu Leu Tyr Arg His Leu Gly Ala
 145 150 155 160

Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val
 165 170 175

Gly Phe Met Ala Gly Met Met Lys Lys Leu Ser Asn Asn Thr Ala Cys
 180 185 190

Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro
 195 200 205

Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys
 210 215 220

Arg His Gly Met Gly Phe Glu Gly Met Arg Val Ser Val Ser Gly Ser
 225 230 235 240

Gly Asn Val Ala Gln Tyr Ala Ile Glu Lys Ala Met Glu Phe Gly Ala
 245 250 255

Arg Val Ile Thr Ala Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ser
 260 265 270

Gly Phe Thr Lys Glu Lys Leu Ala Arg Leu Ile Glu Ile Lys Ala Ser
 275 280 285

Arg Asp Gly Arg Val Ala Asp Tyr Ala Lys Glu Phe Gly Leu Val Tyr
 290 295 300

Leu Glu Gly Gln Gln Pro Trp Ser Leu Pro Val Asp Ile Ala Leu Pro
 305 310 315 320

Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile
 325 330 335

Ala Asn Gly Val Lys Ala Val Ala Glu Gly Ala Asn Met Pro Thr Thr
 340 345 350

Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro
 355 360 365

Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met
 370 375 380

Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala
 385 390 395 400

Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His
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Met Asp Gln Thr Tyr Ser Leu Glu Ser Phe Leu Asn His Val Gln Lys
1          5          10          15

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Arg Asp Pro Asn Gln Thr Glu Phe Ala Gln Ala Val Arg Glu Val Met
20          25          30

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Thr Thr Leu Trp Pro Phe Leu Glu Gln Asn Pro Lys Tyr Arg Gln Met
35          40          45

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Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg
50          55          60

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Val Val Trp Val Asp Asp Arg Asn Gln Ile Gln Val Asn Arg Ala Trp
65          70          75          80

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Arg Val Gln Phe Ser Ser Ala Ile Gly Pro Tyr Leu Gly Gly Met Arg
85          90          95

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Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu
100         105         110

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Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys
115         120         125

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Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Gly Glu Val Met
 130 135 140

Arg Phe Cys Gln Ala Leu Met Thr Glu Leu Tyr Arg His Leu Gly Ala
 145 150 155 160

Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val
 165 170 175

Gly Phe Met Ala Gly Met Met Lys Lys Leu Ser Asn Asn Thr Ala Cys
 180 185 190

Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro
 195 200 205

Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys
 210 215 220

Arg His Gly Met Gly Phe Glu Gly Met Arg Val Ser Val Ser Gly Ser
 225 230 235 240

Gly Asn Val Ala Gln Tyr Ala Ile Glu Lys Ala Met Glu Phe Gly Ala
 245 250 255

Arg Val Ile Thr Ala Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ser
 260 265 270

Gly Phe Thr Lys Glu Lys Leu Ala Arg Leu Ile Glu Ile Lys Ala Ser
 275 280 285

Arg Asp Gly Arg Val Ala Asp Tyr Ala Lys Glu Phe Gly Leu Val Tyr
 290 295 300

Leu Glu Gly Gln Gln Pro Trp Ser Leu Pro Val Asp Ile Ala Leu Pro
 305 310 315 320

Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile
 325 330 335

Ala Asn Gly Val Lys Ala Val Ala Glu Gly Ala Asn Met Pro Thr Thr
 340 345 350

Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro
 355 360 365

Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met
 370 375 380

Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala
 385 390 395 400

Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His
 405 410 415

Gly Gly Glu Gly Glu Gln Thr Asn Tyr Val Gln Gly Ala Asn Ile Ala
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Gly Phe Val Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
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35 40 45

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
50 55 60

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
85 90 95

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
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Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

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 <213> Bacillus subtilis

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 35 40 45

Glu Asn Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly
 50 55 60

Met Thr Tyr Lys Asp Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80

Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Glu Met Phe
 85 90 95

Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
 100 105 110

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile His Asp
 115 120 125

Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly
 130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala
 145 150 155 160

Ala Ala Lys Ala Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Thr Ile
 165 170 175

Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu
 180 185 190

His Glu Glu Gly Ala Asn Leu Ile Val Thr Asp Ile Asn Lys Gln Ser
 195 200 205

Val Gln Arg Ala Val Glu Asp Phe Gly Ala Arg Ala Val Asp Pro Glu
 210 215 220

Glu Ile Tyr Ser Gln Glu Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly
 225 230 235 240

Ala Thr Ile Asn Asp Asp Thr Ile Lys Gln Leu Lys Ala Lys Val Ile
 245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Gln
260 265 270

Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala
275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Ala Glu
290 295 300

Arg Ala Leu Lys Lys Val Glu Gly Ile Tyr Gly Asn Ile Glu Arg Val
305 310 315 320

Leu Glu Ile Ser Gln Arg Asp Gly Ile Pro Thr Tyr Leu Ala Ala Asp
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ggagccacaa ggctttatcc ttatatcaat gaagaagccg ccttaagaga tgctttgcgt 180
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 <213> Nostoc sp.

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 20 25 30

Asp Thr Thr Leu Gly Pro Ala Met Gly Ala Thr Arg Leu Tyr Pro Tyr
 35 40 45

Ile Asn Glu Glu Ala Ala Leu Arg Asp Ala Leu Arg Leu Ser Arg Gly
 50 55 60

Met Thr Tyr Lys Ala Ala Cys Ala Asn Ile Pro Ala Gly Gly Gly Lys
 65 70 75 80

Ala Val Ile Ile Ala Asn Pro Glu Asp Lys Thr Asp Glu Met Leu Arg
 85 90 95

Ala Tyr Gly Arg Phe Val Glu Ser Leu Lys Gly Arg Phe Ile Thr Gly
 100 105 110

Gln Asp Val Asn Ile Thr Pro Gln Asp Val Arg Thr Ile Lys Gln Glu
 115 120 125

Thr Asn Tyr Val Val Gly Val Glu Glu Lys Ser Gly Gly Pro Ala Pro
 130 135 140

Ile Thr Ala Leu Gly Val Phe Leu Gly Ile Lys Ala Ala Val Glu Phe
 145 150 155 160

Arg Trp Gln Thr Lys Asn Ile Glu Gly Met Thr Val Ala Val Gln Gly
 165 170 175

Leu Gly Asn Val Gly Gln Asn Leu Cys Arg His Leu His Glu Asn Gly
 180 185 190

Ile Lys Leu Ile Val Ala Asp Phe Ser Ser Glu Lys Thr Ala Glu Ile
 195 200 205

Lys His Leu Phe Gly Ala Thr Val Val Glu Pro Asp Glu Ile Tyr Ser
 210 215 220

Gln Asn Val Asp Ile Phe Ser Pro Cys Ala Met Gly Gly Ile Ile Asn
 225 230 235 240

Ser Gln Thr Ile Pro Gln Leu Gln Ala Lys Ile Ile Ala Gly Ala Ala
 245 250 255

Asn Asn Gln Leu Asp Asn Glu Arg Leu His Gly Gln Arg Leu Val Glu
 260 265 270

Lys Asp Ile Leu Tyr Cys Pro Asp Tyr Val Ile Asn Ala Gly Gly Ile
 275 280 285

Ile Asn Val Tyr Asn Glu Met Ile Gly Tyr Glu Glu Asp Lys Ala Phe
 290 295 300

Lys Gln Val Asn Asn Ile Tyr Asp Thr Leu Leu Ala Ile Phe Asn Ile
 305 310 315 320

Ala Gln Gln Gln Ser Ile Thr Thr Asn Asp Ala Ser Lys Arg Leu Ala
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Asp Glu Arg Ile Met Lys Ala Arg Ile Asn Lys Asn Gln Leu Ile Ala
 340 345 350

Ala

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 <213> *Shewanella oneidensis*

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Ala Glu Asp Val Gly Thr Thr Thr Ala Asp Ile Met Ile Ala His Gln
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Glu Thr Pro Tyr Met Ala Gly Leu Glu Gly Lys Ser Gly Asp Pro Ser
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Pro Phe Thr Ala Leu Gly Thr Tyr Leu Gly Ile Lys Ala Ala Val Lys
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His Lys Leu Asp Leu Asp Ser Leu Lys Gly Leu Lys Ile Ala Val Gln
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Gly Val Gly His Val Gly Tyr Tyr Leu Cys Lys His Leu His Glu Glu
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 245 250 255

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Met Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Ile
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Ile Asn Val Ser Phe Glu Lys Asp Tyr Asp Ala Ala Lys Ser Glu Ala
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 Leu Leu Asp Arg Leu Ile Glu Pro Glu Arg Met Ile Ile Phe Arg Val
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 Ala Trp Val Asp Asp Arg Gly Glu Val Lys Val Asn Arg Gly Tyr Arg
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 Ile Gln Tyr Asn Ser Ala Ile Gly Pro Tyr Lys Gly Gly Thr Arg Phe
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 His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Ala Phe Glu Gln
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 Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly
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 Phe Thr Gly Lys Gly Leu Thr Phe Gly Gly Ser Leu Leu Arg Pro Glu
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Ser Gly Cys Ser Leu Lys Gly Met Arg Val Ser Val Ser Gly Ser Gly
 225 230 235 240

Asn Val Ala Gln Phe Ala Ile Asp Lys Ala Met Ser Leu Gly Ala Lys
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Val Val Thr Val Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ala Gly
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Phe Thr Pro Glu Lys Leu Ala Ile Leu Ala Glu Val Lys Asn Arg Leu
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Tyr Gly Arg Val Asn Glu Phe Ala Glu Arg Val Glu Ala Gln Phe Leu
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Gly Ala Val Glu Arg Phe His His Ala Lys Val Leu Phe Ala Pro Gly
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Gln Gln Ala Met Arg Leu Ser Trp Thr Ser Gly Glu Val Asp Met Arg
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Leu Gln Glu Ile Met Arg Ala Ile His His Ser Cys Thr Glu Tyr Gly
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O'Neill, Julia P.
Smith, Hong Q.

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<151> 2004-09-23

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Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg
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Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys
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Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Gly Glu Val Met
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Arg Phe Cys Gln Ala Leu Met Thr Glu Leu Tyr Arg His Leu Gly Ala
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Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val
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Gly Phe Met Ala Gly Met Met Lys Lys Leu Ser Asn Asn Thr Ala Cys
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Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro
 195 200 205

Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys
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Arg His Gly Met Gly Phe Glu Gly Met Arg Val Ser Val Ser Gly Ser
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Gly Phe Thr Lys Glu Lys Leu Ala Arg Leu Ile Glu Ile Lys Ala Ser
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Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile
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Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro
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Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met
 370 375 380

Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala
 385 390 395 400

Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His
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Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg
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Val Val Trp Val Asp Asp Arg Asn Gln Ile Gln Val Asn Arg Ala Trp
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Arg Val Gln Phe Ser Ser Ala Ile Gly Pro Tyr Leu Gly Gly Met Arg
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Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu
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Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys
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Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro
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Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys
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Gly Asn Val Ala Gln Tyr Ala Ile Glu Lys Ala Met Glu Phe Gly Ala
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Arg Asp Gly Arg Val Ala Asp Tyr Ala Lys Glu Phe Gly Leu Val Tyr
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Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile
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Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala
 385 390 395 400

Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His
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Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
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Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65 70 75 80

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
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Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
100 105 110

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
115 120 125

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
130 135 140

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
 145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
 165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
 180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
 195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
 210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
 225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
 245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
 260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
 290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
 305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
 325 330 335

Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
 340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 355 360 365

<210> 7

<211> 1098
 <212> DNA
 <213> Bacillus subtilis

<400> 7
 atggaacttt ttaaataatat ggagaaatac gattatgaac aattagtatt ctgccaagat 60
 gaacaatcag gcttaaaagc gattatcgca attcatgata caacgcttgg tccggcgctt 120
 ggcggaacga gaatgtggac atatgaaaat gaagaagcgg caattgaaga cgcgctcaga 180
 ctggcaagag gcatgaccta taaagacgcg gctgcaggcc taaaccttgg cggcggaaaa 240
 acagtaataa tcggcgatcc acgcaaagac aaaaatgaag aaatgttccg cgcgtttggc 300
 cgctatattc aaggactgaa cggcagatac attacagctg aagatgtggg tacaacggtt 360
 gaggatatgg acattattca tgatgaaaca gactatgtca cagggatttc tcctgctttc 420
 ggctcttctg gaaatccatc tccagttaca gcgtacgggg tgtacagagg aatgaaagca 480
 gccgctaaag ctgctttcgg aaccgactct cttgaaggga aaaccatcgc tgtacagggg 540
 gtagggaatg tggcctacaa cctatgccgc cacctgcatg aagaaggggc aaacttaatc 600
 gttacggata tcaacaaaca gtcagtacag cgcgcagttg aagattttgg cgcccgtgcg 660
 gttgatccgg aagagattta ttcacaagag tgcgatattt atgctccgtg cgcccttgga 720
 gcgacaatca acgacgacac cattaaacag ctgaaggcga aagtcatcgc ggggtgcggct 780
 aataaccaat taaaagaaac gcgccatggc gatcaaattc acgaaatggg tatcgtttac 840
 gcaccggatt atgtcattaa cgcaggcggc gtgatcaacg tggcagatga gctttacggc 900
 tataatgcag aacgtgcatt gaaaaaagtt gaaggcattt acggcaatat tgagcgtgta 960
 cttgagattt ctcagcgtga cggcattcca acatatttag cagctgaccg cttggcagag 1020
 gaacggattg aacgcatgcg ccgctcaaga agccagtttt tgcaaaacgg ccacagtgta 1080
 ttaagcagac gttaatag 1098

<210> 8
 <211> 364
 <212> PRT
 <213> Bacillus subtilis

<400> 8
 Met Glu Leu Phe Lys Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val
 1 5 10 15
 Phe Cys Gln Asp Glu Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
 35 40 45

Glu Asn Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly
 50 55 60

Met Thr Tyr Lys Asp Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
 65 70 75 80

Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Glu Met Phe
 85 90 95

Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
 100 105 110

Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile His Asp
 115 120 125

Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly
 130 135 140

Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala
 145 150 155 160

Ala Ala Lys Ala Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Thr Ile
 165 170 175

Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu
 180 185 190

His Glu Glu Gly Ala Asn Leu Ile Val Thr Asp Ile Asn Lys Gln Ser
 195 200 205

Val Gln Arg Ala Val Glu Asp Phe Gly Ala Arg Ala Val Asp Pro Glu
 210 215 220

Glu Ile Tyr Ser Gln Glu Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly
 225 230 235 240

Ala Thr Ile Asn Asp Asp Thr Ile Lys Gln Leu Lys Ala Lys Val Ile
 245 250 255

Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Gln
260 265 270

Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala
275 280 285

Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Ala Glu
290 295 300

Arg Ala Leu Lys Lys Val Glu Gly Ile Tyr Gly Asn Ile Glu Arg Val
305 310 315 320

Leu Glu Ile Ser Gln Arg Asp Gly Ile Pro Thr Tyr Leu Ala Ala Asp
325 330 335

Arg Leu Ala Glu Glu Arg Ile Glu Arg Met Arg Arg Ser Arg Ser Gln
340 345 350

Phe Leu Gln Asn Gly His Ser Val Leu Ser Arg Arg
355 360

<210> 9
<211> 1062
<212> DNA
<213> Nostoc sp.

<400> 9
atgcagctat ttgaaactgt tagagaaatg ggacatgagc aagtactcta ctgtcatgga 60
aaaaatccag atattagagc aataattgcc atccatgaca ccacattagg cccagcaatg 120
ggagccacaa ggctttatcc ttatatcaat gaagaagccg ccttaagaga tgctttgcgt 180
ttgagtcggg ggatgactta taaagcagct tgcgctaaca ttcccgcagg cggaggcaaa 240
gccgttatta ttgccaatcc cgaagataaa acagatgaaa tgttgagagc ttatggacgc 300
tttgtggaag gtctcaaagg tagatttatt accgggcaag atgtgaatat cactccacaa 360
gatgtccgca caattaaaca agaaaccaat tatgtagttg gtgtggaaga aaaatctggt 420
gggcctgctc ctatcacagc tttaggcgta tttttaggta ttaaagctgc tgtagaattt 480
cgctggcaaa ctaaaaaatat tgaagggatg acagttgccg ttcaaggttt aggaaatgtt 540
ggtcagaatc tctgccgaca cttacatgaa aatgggtataa agcttatagt tgctgatttt 600
agttctgaaa aaacagcaga aataaaaacac ctttttggtg ctacagtagt agagccagat 660

gaaatttact cacaaaatgt agacatattt tctccctgtg ctatgggagg aattattaac 720
 agtcaaacaa ttccccaact acaagccaaa attattgctg gtgctgccaa taaccagtta 780
 gataatgagc gtctgcatgg tcaaagatta gtagaaaaag atatcctcta ctgtcctgat 840
 tatgtaatca atgctgggtgg tatcatcaac gtttataacg aaatgattgg ctatgaagaa 900
 gataaggcct tcaagcaagt taataatatt tacgacacat tattagcaat tttcaatatt 960
 gctcaacaac aaagcattac tactaatgat gcttcaaaac ggcttgacaga tgaaaggatt 1020
 atgaaggcga gaatcaataa aaatcaacta attgctgcct aa 1062

<210> 10
 <211> 353
 <212> PRT
 <213> Nostoc sp.

<400> 10

Met Gln Leu Phe Glu Thr Val Arg Glu Met Gly His Glu Gln Val Leu
 1 5 10 15

Tyr Cys His Gly Lys Asn Pro Asp Ile Arg Ala Ile Ile Ala Ile His
 20 25 30

Asp Thr Thr Leu Gly Pro Ala Met Gly Ala Thr Arg Leu Tyr Pro Tyr
 35 40 45

Ile Asn Glu Glu Ala Ala Leu Arg Asp Ala Leu Arg Leu Ser Arg Gly
 50 55 60

Met Thr Tyr Lys Ala Ala Cys Ala Asn Ile Pro Ala Gly Gly Gly Lys
 65 70 75 80

Ala Val Ile Ile Ala Asn Pro Glu Asp Lys Thr Asp Glu Met Leu Arg
 85 90 95

Ala Tyr Gly Arg Phe Val Glu Ser Leu Lys Gly Arg Phe Ile Thr Gly
 100 105 110

Gln Asp Val Asn Ile Thr Pro Gln Asp Val Arg Thr Ile Lys Gln Glu
 115 120 125

Thr Asn Tyr Val Val Gly Val Glu Glu Lys Ser Gly Gly Pro Ala Pro
 130 135 140

Ile Thr Ala Leu Gly Val Phe Leu Gly Ile Lys Ala Ala Val Glu Phe
 145 150 155 160

Arg Trp Gln Thr Lys Asn Ile Glu Gly Met Thr Val Ala Val Gln Gly
 165 170 175

Leu Gly Asn Val Gly Gln Asn Leu Cys Arg His Leu His Glu Asn Gly
 180 185 190

Ile Lys Leu Ile Val Ala Asp Phe Ser Ser Glu Lys Thr Ala Glu Ile
 195 200 205

Lys His Leu Phe Gly Ala Thr Val Val Glu Pro Asp Glu Ile Tyr Ser
 210 215 220

Gln Asn Val Asp Ile Phe Ser Pro Cys Ala Met Gly Gly Ile Ile Asn
 225 230 235 240

Ser Gln Thr Ile Pro Gln Leu Gln Ala Lys Ile Ile Ala Gly Ala Ala
 245 250 255

Asn Asn Gln Leu Asp Asn Glu Arg Leu His Gly Gln Arg Leu Val Glu
 260 265 270

Lys Asp Ile Leu Tyr Cys Pro Asp Tyr Val Ile Asn Ala Gly Gly Ile
 275 280 285

Ile Asn Val Tyr Asn Glu Met Ile Gly Tyr Glu Glu Asp Lys Ala Phe
 290 295 300

Lys Gln Val Asn Asn Ile Tyr Asp Thr Leu Leu Ala Ile Phe Asn Ile
 305 310 315 320

Ala Gln Gln Gln Ser Ile Thr Thr Asn Asp Ala Ser Lys Arg Leu Ala
 325 330 335

Asp Glu Arg Ile Met Lys Ala Arg Ile Asn Lys Asn Gln Leu Ile Ala
 340 345 350

Ala

<210> 11
 <211> 1044
 <212> DNA
 <213> *Shewanella oneidensis*

<400> 11
 atggctgtat ttaatcatgt atcctttgat gagcatgaac aggtcgtatt ctgtcatgat 60
 aaagaaagtg gcttaaaagc cattattgcc atccataata ccaatttagg ccctgctgtg 120
 ggtggatgcc ggatgtggaa ctaccaatcc gatgacgaag ccctgacaga cgtattacgc 180
 ctctcccgtg gtatgactta caaaaacgcg ctcgctgggt taaccatggg cgggtggtaaa 240
 tcagtgatta ttgccgatcc taagcgccct gaccggaag ccctcttccg tgcttttggc 300
 cgttttatca atagtctcgg tggacgttac tattccgcag aagacgttgg caccacgaca 360
 gctgatatta tgatcgccca tcaagaaacg ccctatatgg cggggcttga aggcaagagt 420
 ggcgatcctt ctccgtttac ggactaggt acttatttag gtatcaaggc cgcggttaaa 480
 cataagctcg atttagacag cttaaagggc cttaagatcg ccgttcaagg tgttggccat 540
 gtgggttatt atctgtgtaa acatctacat gaagaagggt cacagctaatt tgttaccgat 600
 attcatcagg cgtcacttga taaagtggct accgactttg gtgctaccgt tgttgcacca 660
 caggatatct acgccaaga cgtcgatgtg tacgccccat gcgcactagg tgcgacctta 720
 aacgatgtta ccctgccact actcaaagct aagattgttg caggttgtgc caacaaccaa 780
 ttagccgaag tacgccatgg cgagcagtta aaagaaatgg gcattcttta tgcgccagat 840
 tatgtgatta acgcgggcgg cattattaac gtatcattcg aaaaagacta tgatgcggcg 900
 aaatcagaag ctaaggtcag agaaatctac aacacgctgc tgaagatttt tgctaaagcc 960
 gatgctgaga accgcacgac aggtgcagta gctgacgaaa tggcccgtgc aatttaccaa 1020
 gcgccaagc ctaatagggc ttag 1044

<210> 12
 <211> 347
 <212> PRT
 <213> *Shewanella oneidensis*

<400> 12
 Met Ala Val Phe Asn His Val Ser Phe Asp Glu His Glu Gln Val Val
 1 5 10 15
 Phe Cys His Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala Ile His
 20 25 30

Asn Thr Asn Leu Gly Pro Ala Val Gly Gly Cys Arg Met Trp Asn Tyr
 35 40 45

Gln Ser Asp Asp Glu Ala Leu Thr Asp Val Leu Arg Leu Ser Arg Gly
 50 55 60

Met Thr Tyr Lys Asn Ala Leu Ala Gly Leu Thr Met Gly Gly Gly Lys
 65 70 75 80

Ser Val Ile Ile Ala Asp Pro Lys Arg Pro Asp Arg Glu Ala Leu Phe
 85 90 95

Arg Ala Phe Gly Arg Phe Ile Asn Ser Leu Gly Gly Arg Tyr Tyr Ser
 100 105 110

Ala Glu Asp Val Gly Thr Thr Thr Ala Asp Ile Met Ile Ala His Gln
 115 120 125

Glu Thr Pro Tyr Met Ala Gly Leu Glu Gly Lys Ser Gly Asp Pro Ser
 130 135 140

Pro Phe Thr Ala Leu Gly Thr Tyr Leu Gly Ile Lys Ala Ala Val Lys
 145 150 155 160

His Lys Leu Asp Leu Asp Ser Leu Lys Gly Leu Lys Ile Ala Val Gln
 165 170 175

Gly Val Gly His Val Gly Tyr Tyr Leu Cys Lys His Leu His Glu Glu
 180 185 190

Gly Ala Gln Leu Ile Val Thr Asp Ile His Gln Ala Ser Leu Asp Lys
 195 200 205

Val Ala Thr Asp Phe Gly Ala Thr Val Val Ala Pro Gln Asp Ile Tyr
 210 215 220

Ala Gln Asp Val Asp Val Tyr Ala Pro Cys Ala Leu Gly Ala Thr Leu
 225 230 235 240

Asn Asp Val Thr Leu Pro Leu Leu Lys Ala Lys Ile Val Ala Gly Cys
 245 250 255

Ala Asn Asn Gln Leu Ala Glu Val Arg His Gly Glu Gln Leu Lys Glu
260 265 270

Met Gly Ile Leu Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly Ile
275 280 285

Ile Asn Val Ser Phe Glu Lys Asp Tyr Asp Ala Ala Lys Ser Glu Ala
290 295 300

Lys Val Arg Glu Ile Tyr Asn Thr Leu Leu Lys Ile Phe Ala Lys Ala
305 310 315 320

Asp Ala Glu Asn Arg Thr Thr Gly Ala Val Ala Asp Glu Met Ala Arg
325 330 335

Ala Ile Tyr Gln Ala Pro Lys Pro Asn Arg Ala
340 345

<210> 13
<211> 1086
<212> DNA
<213> Streptomyces avermitilis

<400> 13
gtgaccgatg tatccgacgg cgtcctgcac accctgttcc gtcggacca gggggggcat 60
gagcaagtgc tgctctgccg ggaccgggcc actggtctca aggccgtcat cgccatccac 120
tccaccgccc tgggccccgc cctcggcggt acgcgcttct acccgtagcg gagcgaggag 180
gaggccgtcg ccgacgcgct gaacctcgcg cgcgggatgt cgtacaagaa cgccatggcc 240
ggcctcgacc acggcgggcg caaggccgtc atcatcgggtg accccgagcg gatcaagacc 300
gaggagctgc tgctggccta cggccgggtc gtggcctcgc tcggcgggcg gtacgtcacc 360
gcgtgcgacg tcggtacgta cgtcgccgac atggacgtcg tggcgcgca gtgccgtgg 420
acgaccgggc gctccccgga gaacggcggc gcgggcgact cctccgtgct gaccgccttc 480
ggtgtcttcc agggcatgcg ggccctccgc cagcacctgt ggggcgaccc gacgctgcgc 540
ggccgcaagg tgggcatcgc gggcgtcggc aaggtcggcc gccacctggt gcggcacctg 600
ctggacgacg gcgcgagggt cgtgatcacg gacgtgcgga ccgactccgt acagcggatc 660
ctcgaccagc acccgacggg cgtcacggcc gtcgcgga ccgacgcgct gatccgggtg 720
gacgggctcg acatctacgc cccgtgcgcg ctcggcgggg ccctgaacga cgactccgtc 780
acggtgctca ccgcaagat cgtgtgcggc gcggccaaca accagctcgc ccacacgggc 840

gtcgagaagg acctcgccga ccgcgggata ctctacgcgc cggactacgt ggtgaacgcg 900
 ggcgggggtca tccaggtcgc cgacgagctg cacggcttcg acttcgaccg gtgcaaggcg 960
 aaggccgcga agatcttcga caccacgctg gccatattcg cacgtgcgaa ggaagacggc 1020
 attccgcccgg ccgccgcggc cgaccggatt gccgagcagc gcatggcgga ggcccgccgg 1080
 ggctga 1086

<210> 14
 <211> 361
 <212> PRT
 <213> Streptomyces avermitilis

<400> 14

Met Thr Asp Val Ser Asp Gly Val Leu His Thr Leu Phe Arg Ser Asp
 1 5 10 15

Gln Gly Gly His Glu Gln Val Val Leu Cys Gln Asp Arg Ala Thr Gly
 20 25 30

Leu Lys Ala Val Ile Ala Ile His Ser Thr Ala Leu Gly Pro Ala Leu
 35 40 45

Gly Gly Thr Arg Phe Tyr Pro Tyr Ala Ser Glu Glu Glu Ala Val Ala
 50 55 60

Asp Ala Leu Asn Leu Ala Arg Gly Met Ser Tyr Lys Asn Ala Met Ala
 65 70 75 80

Gly Leu Asp His Gly Gly Gly Lys Ala Val Ile Ile Gly Asp Pro Glu
 85 90 95

Arg Ile Lys Thr Glu Glu Leu Leu Leu Ala Tyr Gly Arg Phe Val Ala
 100 105 110

Ser Leu Gly Gly Arg Tyr Val Thr Ala Cys Asp Val Gly Thr Tyr Val
 115 120 125

Ala Asp Met Asp Val Val Ala Arg Glu Cys Arg Trp Thr Thr Gly Arg
 130 135 140

Ser Pro Glu Asn Gly Gly Ala Gly Asp Ser Ser Val Leu Thr Ala Phe
 145 150 155 160

Gly Val Phe Gln Gly Met Arg Ala Ser Ala Gln His Leu Trp Gly Asp
165 170 175

Pro Thr Leu Arg Gly Arg Lys Val Gly Ile Ala Gly Val Gly Lys Val
180 185 190

Gly Arg His Leu Val Arg His Leu Leu Asp Asp Gly Ala Glu Val Val
195 200 205

Ile Thr Asp Val Arg Thr Asp Ser Val Gln Arg Ile Leu Asp Gln His
210 215 220

Pro Thr Gly Val Thr Ala Val Ala Asp Thr Asp Ala Leu Ile Arg Val
225 230 235 240

Asp Gly Leu Asp Ile Tyr Ala Pro Cys Ala Leu Gly Gly Ala Leu Asn
245 250 255

Asp Asp Ser Val Thr Val Leu Thr Ala Lys Ile Val Cys Gly Ala Ala
260 265 270

Asn Asn Gln Leu Ala His Thr Gly Val Glu Lys Asp Leu Ala Asp Arg
275 280 285

Gly Ile Leu Tyr Ala Pro Asp Tyr Val Val Asn Ala Gly Gly Val Ile
290 295 300

Gln Val Ala Asp Glu Leu His Gly Phe Asp Phe Asp Arg Cys Lys Ala
305 310 315 320

Lys Ala Ala Lys Ile Phe Asp Thr Thr Leu Ala Ile Phe Ala Arg Ala
325 330 335

Lys Glu Asp Gly Ile Pro Pro Ala Ala Ala Ala Asp Arg Ile Ala Glu
340 345 350

Gln Arg Met Ala Glu Ala Arg Arg Gly
355 360

<210> 15
<211> 1347
<212> DNA

<213> Nitrosomonas europaea

<400> 15

atgaaataca acagtatcga ggaattcaag aattatgttt ccgaaaggaa tccagggcaa	60
cccgaattcc tgcaggccgt ttcagaagtc attgaaagct tgtggccttt tatcgtcgat	120
cattctcgtt acgctgagca ggggttgctg gatcggctga tcgagccgga gcgcatgac	180
atattccggg tggcgtgggt ggatgatcgg ggtgaagtca aggtcaatcg ggggtaccgc	240
attcaatata attcggcgat cggcccatac aaggggggta cgcgcttcca tccgtcagtc	300
aacctttcca ttctcaaatt ccttgcattt gagcagactt tcaagaatgc actgacaaca	360
ttgccgatgg gaggaggcaa ggggtggatcg gattttgatc ccaagggtaa aagtcccgg	420
gaaatcatgc gcttctgcca agcgtatgcg gccgaactgt tccggcatgt cgggtcggat	480
acggatgtac ctgccggaga catcgggtgtg ggcggacggg aagtcggcta catggctggt	540
atggtcaaga agctgaccaa ccgttcggac tgtgtattta ccggcaaagg attgacctc	600
gggggatcgc tgctgcggcc ggaagctacc gggtaggtc tggctctattt tgccgaagag	660
atgctgaatc actccggttg ttcatgaaa ggcattgcggg tatccgtatc cggttccggg	720
aacgtggcac agtttgccat tgacaaggcc atgtcgctgg gtgcaaagt agtcacgggt	780
tcagattcga gtggtacggt ggtggatgaa gccggtttta caccagaaaa actggcaatt	840
ctggccgaag tcaagaatcg tctctacggg cgtgtcaatg aatttgctga acgggtggaa	900
gcacagttcc ttccgggtga aaaaccgtgg catgtgccgg tggatgtcgc ttgacctgt	960
gcgaccaga atgaactgaa cgaaaacgac gccgcaatac tgatcaggaa tgggtgcgaat	1020
tgtgtggccg aggggtgcaa tatgccatgc actgcaggtg ccgtggaacg attccatcat	1080
gcgaaagtac tgtttgcacc tggcaaggcg agcaacgcag gcggagtggc tacctcgggt	1140
ctggaaatga gccagcaggc catgcgactt tcctggacga gcggagaagt cgatatgcgg	1200
ttacaggaaa tcatgcgtgc cattcatcat tcctgcaccg aatacggcaa gaagcctgac	1260
ggtagcgtca actatgtgga tgggtgccaat gttgccggat ttgtgaaagt ggccgaggca	1320
atgctggcgc aaggggtgat ctgataa	1347

<210> 16

<211> 447

<212> PRT

<213> Nitrosomonas europaea

<400> 16

Met	Lys	Tyr	Asn	Ser	Ile	Glu	Glu	Phe	Lys	Asn	Tyr	Val	Ser	Glu	Arg	1	5	10	15
Asn	Pro	Gly	Gln	Pro	Glu	Phe	Leu	Gln	Ala	Val	Ser	Glu	Val	Ile	Glu	20	25	30	
Ser	Leu	Trp	Pro	Phe	Ile	Val	Asp	His	Ser	Arg	Tyr	Ala	Glu	Gln	Gly	35	40	45	
Leu	Leu	Asp	Arg	Leu	Ile	Glu	Pro	Glu	Arg	Met	Ile	Ile	Phe	Arg	Val	50	55	60	
Ala	Trp	Val	Asp	Asp	Arg	Gly	Glu	Val	Lys	Val	Asn	Arg	Gly	Tyr	Arg	65	70	75	80
Ile	Gln	Tyr	Asn	Ser	Ala	Ile	Gly	Pro	Tyr	Lys	Gly	Gly	Thr	Arg	Phe	85	90	95	
His	Pro	Ser	Val	Asn	Leu	Ser	Ile	Leu	Lys	Phe	Leu	Ala	Phe	Glu	Gln	100	105	110	
Thr	Phe	Lys	Asn	Ala	Leu	Thr	Thr	Leu	Pro	Met	Gly	Gly	Gly	Lys	Gly	115	120	125	
Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Pro	Gly	Glu	Ile	Met	Arg	130	135	140	
Phe	Cys	Gln	Ala	Tyr	Ala	Ala	Glu	Leu	Phe	Arg	His	Val	Gly	Ala	Asp	145	150	155	160
Thr	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Val	Gly	165	170	175	
Tyr	Met	Ala	Gly	Met	Val	Lys	Lys	Leu	Thr	Asn	Arg	Ser	Asp	Cys	Val	180	185	190	
Phe	Thr	Gly	Lys	Gly	Leu	Thr	Phe	Gly	Gly	Ser	Leu	Leu	Arg	Pro	Glu	195	200	205	
Ala	Thr	Gly	Tyr	Gly	Leu	Val	Tyr	Phe	Ala	Glu	Glu	Met	Leu	Asn	His	210	215	220	

Ser Gly Cys Ser Leu Lys Gly Met Arg Val Ser Val Ser Gly Ser Gly
 225 230 235 240

Asn Val Ala Gln Phe Ala Ile Asp Lys Ala Met Ser Leu Gly Ala Lys
 245 250 255

Val Val Thr Val Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ala Gly
 260 265 270

Phe Thr Pro Glu Lys Leu Ala Ile Leu Ala Glu Val Lys Asn Arg Leu
 275 280 285

Tyr Gly Arg Val Asn Glu Phe Ala Glu Arg Val Glu Ala Gln Phe Leu
 290 295 300

Pro Gly Glu Lys Pro Trp His Val Pro Val Asp Val Ala Leu Pro Cys
 305 310 315 320

Ala Thr Gln Asn Glu Leu Asn Glu Asn Asp Ala Ala Ile Leu Ile Arg
 325 330 335

Asn Gly Ala Asn Cys Val Ala Glu Gly Ala Asn Met Pro Cys Thr Ala
 340 345 350

Gly Ala Val Glu Arg Phe His His Ala Lys Val Leu Phe Ala Pro Gly
 355 360 365

Lys Ala Ser Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met Ser
 370 375 380

Gln Gln Ala Met Arg Leu Ser Trp Thr Ser Gly Glu Val Asp Met Arg
 385 390 395 400

Leu Gln Glu Ile Met Arg Ala Ile His His Ser Cys Thr Glu Tyr Gly
 405 410 415

Lys Lys Pro Asp Gly Thr Val Asn Tyr Val Asp Gly Ala Asn Val Ala
 420 425 430

Gly Phe Val Lys Val Ala Glu Ala Met Leu Ala Gln Gly Val Ile
 435 440 445